Amendments to the Specification:

Replace the original Sequence Listing with an amended substitute Sequence Listing filed herewith.

Please amend the paragraph beginning at page 18, line 14, as follows:

Chromosome localizations of each AtTLP genes were determined using Map View ~~(www.arabidopsis.org/servlets/mapper)~~ available at the website of arabidopsis.org/servlets/mapper (Huala et al., 2001, Nucleic Acids Res 29: 102-105). It was found that the genes were not evenly distributed on chromosomes I, II, III, and V. Seven genes (AtTLPs 1, 4, 5, 6, 7, 8, and 10) were located on chromosome I, and two genes (AtTLPs 2 and 3) were located on chromosomes II. The other two, AtTLPs 9 and 11, were located on chromosomes II, III respectively. Although most of the AtTLP genes were located on chromosome I, no local tandem repeats or gene clusters were identified.

Please amend the paragraph beginning at page 19, line 15, as follows:

Although the expression of AtTLP1, 2, 3, 6, 7, 9, 10 and 11 is present in all tissues tested, the possibility that these genes are expressed with cell type specificity could not be excluded. It is possible that differential expression of these AtTLP genes could only be observed when internal developmental programming was altered or specific environmental stimuli were applied to the plants. To test this hypothesis, the public Arabidopsis Functional Genomics Consortium (AFGC) microarray expression database (the Stanford Microarray Database, ~~genome-www5.~~ available at the website of stanford.edu/MicroArray/SMD/) (Wu et al., 2001, Plant Physiol Biochem 39: 917-926) was searched. Twofold expression was used as the difference cutoff. Based on the search, the expression profiles of DNA fragments corresponding to AtTLP2, 7, 9 and 10 were summarized in Table 2 below.

Please amend the first sentence below Table 3 at page 20, as follows

[a] These data are obtained from ~~http://~~ the website of afgc.stanford.edu/afgc_html/site2.htm

Please amend the paragraph beginning at page 23, line 4, as follows:

To identify attlp9 T-DNA insertion mutant, AtTLP9 (At3g06380) was used to search the T-DNA Express database at ~~http://~~ the website of signal.salk.edu/cgi-bin/tdnaexpress. Two attlp9 T-DNA insertion mutants (ABRC seed stock SALK_016678 and 051138) were identified and designated as attlp9-1 and attlp9-2. T3 seeds of attlp9-1 and attlp9-2 were obtained from the Arabidopsis Biological Resource Center (Ohio State University, Columbus). The position of the T-DNA within the AtTLP9 gene was re-confirmed by sequencing a PCR-amplified fragment amplified by primer pairs corresponding to the T-DNA left borders and the AtTLP9 gene specific primer. The following primer pairs were used for attlp9-1 and attlp9-2 specific amplification,

attlp9-1: N1, 5' -ATGACGTTCCGAAGTTTACTC- 3' (SEQ ID NO:45);

LBa1, 5' -TGGTTCACGTAGTGGGCCATC- 3' (SEQ ID NO:46);

attlp9-2: C1, 5' -TTATTCACAGGCAATTCTGGT- 3' (SEQ ID NO:47); and

LBa1, 5' -TGGTTCACGTAGTGGGCCATC- 3' (SEQ ID NO:[[48]]46).

Please amend the paragraph beginning at page 25, line 30, as follows:

Real-time PCR experiments were conducted to quantify AtTLP9 transcript levels at seed maturation, seed germination, and early development stage. UBQ10 was used as the endogenous control (Norris et al., 1993, Plant. Mol. Biol. 21: 895-906). Primers were designed using Primer Express 1.0 software (Applied Biosystems). The primers used were:

AtTLP9 forward primer, 5'-TAGGCCACACCGTGTAGTTCA-3'; (SEQ ID NO:48)

AtTLP9 reverse primer, 5'-CGTCAACAGTCTCAACCCTAATCA-3'; (SEQ ID NO:49)

UBQ10 forward primer, 5'- AGAAGTTCAATGTTTCGTTTCATGTAA -3' (SEQ ID NO:50); and